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<110> Gilbert, Michel
Wakarchuk, Warren W.
National Research Council of Canada

<120> Campylobacter Glycosyltransferases for Biosynthesis of
Gangliosides and Ganglioside Mimics

<130> 019633-000111US

<140> US 09/816,028

<141> 2001-03-21

<150> US 60/118,213

<151> 1999-02-01

<150> US 09/495,406

<151> 2000-01-31

<160> 49

<170> PatentIn Ver. 2.1

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<223> 11.5 kb PCR product from C. jejuni OH4384
including LOS biosynthesis locus

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Campylobacter sialyltransferase II (cstII) from *C. jejuni*
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biosynthesis locus)

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gat tat ttt cct gat gct cat ttg gga tat gat ttt ttc aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gat ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Asp Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtt tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat act aaa caa aaa aat ctt tta aaa ttg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
aat ttt aaa aat gat aat tca cac tat atc gga cat agt aaa aat aca	576
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

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aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
                245                250                255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
                260                265                270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
                275                280                285

aaa gga aaa taa 876
Lys Gly Lys
290

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<210> 3
<211> 291
<212> PRT
<213> Campylobacter jejuni

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<220>
<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
      Campylobacter sialyltransferase II (cstII) from C. jejuni
      strain OH4384 (ORF 7a of lipooligosaccharide (LOS)
      biosynthesis locus)

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<400> 3
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1          5          10          15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
          20          25          30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
          35          40          45
Phe Tyr Asn Pro Ile Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
          50          55          60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
          65          70          75          80
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
          85          90          95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
          100         105         110
Lys Asp Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
          115         120         125
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
          130         135         140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
          145         150         155         160
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro
          165         170         175
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr
          180         185         190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
          195         200         205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
          210         215         220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
          225         230         235         240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
          245         250         255

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Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
260 265 270
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
275 280 285
Lys Gly Lys
290

<210> 4
<211> 876
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(876)
<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
Campylobacter sialyltransferase II (cstII) from C. jejuni
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)
biosynthesis locus)

<400> 4
atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
1 5 10 15
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgc aat caa 96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
20 25 30
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa ttc aaa gca gta 144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val
35 40 45
ttt tac aat cct ggt ctt ttt ttt gaa caa tac tac act tta aaa cat 192
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
50 55 60
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
65 70 75 80
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
85 90 95
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
100 105 110
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ctc aat caa 384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln
115 120 125
aga att acc tca gga gtc tat atg tgt gca gta gct ata gcc cta gga 432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
130 135 140

tac aaa gaa att tat ctt tct gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa ctg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 5

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
Campylobacter sialyltransferase II (cstII) from C. jejuni
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)
biosynthesis locus)

<400> 5

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val	
35 40 45	
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	

Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 6
 <211> 876
 <212> DNA
 <213> Campylobacter jejuni

 <220>
 <221> CDS
 <222> (1)..(876)
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (cstII) from C. jejuni serotype O:41

<400> 6
 atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15

 gat tat tca aga cta cca aat gat ttt gat gta ttt aga tgc aat caa 96
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30

 ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gta 144
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
 35 40 45

 ttt tac aat cct agt ctt ttt ttt gaa caa tac tac act tta aaa cat 192
 Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60

tta atc caa aat caa gaa tat gag acc gaa cta atc atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
ttt aac caa gct cat cta gaa aat caa aat ttt gta aaa act ttt tac	288
Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttc aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttc aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgc aca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat gga tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa aaa aat ctt tta aaa ttg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
aat ttt aaa aat gat aat tca cac tat atc gga cat agt aaa aat aca	576
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac gaa ata aag cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu	
195 200 205	
tat tgt tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tat act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt aca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 7
 <211> 291
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (cstII) from C. jejuni serotype O:41

<400> 7
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
 35 40 45
 Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 8
 <211> 876
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(876)
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni O:19

<400> 8

atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att	48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa	96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg	144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat	192
Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac	288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tcg cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

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aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
                245                250                255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
                260                265                270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
                275                280                285

aaa gga aaa taa 876
Lys Gly Lys
    290

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<210> 9
<211> 291
<212> PRT
<213> Campylobacter jejuni

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<220>
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
      (CstII) from C. jejuni O:19

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<400> 9
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1          5          10          15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20          25          30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
 35          40          45
Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50          55          60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65          70          75          80
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85          90          95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
100          105          110
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
115          120          125
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
130          135          140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
145          150          155          160
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
165          170          175
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
180          185          190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
195          200          205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
210          215          220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
225          230          235          240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
245          250          255
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
260          265          270

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Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 10
 <211> 294
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni strain NCTC 11168

<400> 10
 Met Ser Met Asn Ile Asn Ala Leu Val Cys Gly Asn Gly Pro Ser Leu
 1 5 10 15
 Lys Asn Ile Asp Tyr Lys Arg Leu Pro Lys Gln Phe Asp Val Phe Arg
 20 25 30
 Cys Asn Gln Phe Tyr Phe Glu Asp Arg Tyr Phe Val Gly Lys Asp Val
 35 40 45
 Lys Tyr Val Phe Phe Asn Pro Phe Val Phe Phe Glu Gln Tyr Tyr Thr
 50 55 60
 Ser Lys Lys Leu Ile Gln Asn Glu Glu Tyr Asn Ile Glu Asn Ile Val
 65 70 75 80
 Cys Ser Thr Ile Asn Leu Glu Tyr Ile Asp Gly Phe Gln Phe Val Asp
 85 90 95
 Asn Phe Glu Leu Tyr Phe Ser Asp Ala Phe Leu Gly His Glu Ile Ile
 100 105 110
 Lys Lys Leu Lys Asp Phe Phe Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr
 115 120 125
 Asn Arg Gln Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Thr Ala Val
 130 135 140
 Ala Leu Gly Tyr Lys Ser Ile Tyr Ile Ser Gly Ile Asp Phe Tyr Gln
 145 150 155 160
 Asp Thr Asn Asn Leu Tyr Ala Phe Asp Asn Asn Lys Lys Asn Leu Leu
 165 170 175
 Asn Lys Cys Thr Gly Phe Lys Asn Gln Lys Phe Lys Phe Ile Asn His
 180 185 190
 Ser Met Ala Cys Asp Leu Gln Ala Leu Asp Tyr Leu Met Lys Arg Tyr
 195 200 205
 Asp Val Asn Ile Tyr Ser Leu Asn Ser Asp Glu Tyr Phe Lys Leu Ala
 210 215 220
 Pro Asp Ile Gly Ser Asp Phe Val Leu Ser Lys Lys Pro Lys Lys Tyr
 225 230 235 240
 Ile Asn Asp Ile Leu Ile Pro Asp Lys Tyr Ala Gln Glu Arg Tyr Tyr
 245 250 255
 Gly Lys Lys Ser Arg Leu Lys Glu Asn Leu His Tyr Lys Leu Ile Lys
 260 265 270
 Asp Leu Ile Arg Leu Pro Ser Asp Ile Lys His Tyr Leu Lys Glu Lys
 275 280 285
 Tyr Ala Asn Lys Asn Arg
 290

<210> 11
 <211> 873
 <212> DNA
 <213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(873)

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni O:4

<400> 11

atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att	48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa	96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg	144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
ttt tac acc cct ggt ttc ttc ttt gag caa tac tac act tta aaa cat	192
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac	288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	

tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa	873
Lys Gly Lys	
290	
<210> 12	
<211> 291	
<212> PRT	
<213> Campylobacter jejuni	
<220>	
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II	
(CstII) from C. jejuni O:4	
<400> 12	
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	

Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 13
 <211> 873
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(873)
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni O:36

<400> 13
 atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15
 gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa 96
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30
 ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa aca gtg 144
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val
 35 40 45
 ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat 192
 Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa 384
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125

aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga 432
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140

 tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca 480
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160

 tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct 528
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175

 gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca 576
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190

 gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta 624
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205

 tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg 672
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220

 cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act 720
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240

 aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255

 aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270

 ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285

 aaa gga aaa 873
 Lys Gly Lys
 290

<210> 14

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni O:36

<400> 14

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30

Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val
 35 40 45
 Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 15
 <211> 1170
 <212> DNA
 <213> *Campylobacter jejuni*

<220>
 <223> glycosyltransferase from *C. jejuni* strain OH4384
 (ORF 4a of lipooligosaccharide (LOS) biosynthesis
 locus)

<400> 15
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 ttagatagcg ttatcaatca aacttatact aacttagaaa tcatacttgt caatgatggg 120
 agcacagatg aacactcact caatattgca aaagaatata ccttaaaaaga taaaagaata 180
 actctttttg ataagaaaaa tgggggttta agttcagcta gaaatatagg tatagaatac 240
 ttttagcggg aatataaatt aaaaaacaaa actcaacata taaaagaaaa ttctttaata 300
 gaatttcaat tggatggtta taatccttat aatatatata aagcatataa aagctctcaa 360
 gcttttaata atgaaaaaga tttaaccaat ttactttacc ctagtataga ttatattata 420
 ttcttagata gtgataatta ttggaaacta aactgcatag aagaatgcgt tataagaatg 480
 aaaaatgtgg atgtattgtg gtttgaccat gattgcacct atgaagacaa tataaaaaat 540
 aagcacaaaa aaacaaggat ggaaattttt gatttttaaaa aagaatgtat aatcactcca 600
 aaagaatatg caaatcgagc attaatgtga ggatctagag atatttcttt tggatggaat 660
 ggaatgattg atttttaattt tttaaagcaa attaaactta aattttataaa ttttattatc 720
 aatgaagata tacacttttg gataattttg tttgctagtg ctaataaaaat ttatgtttta 780
 tcacaaaagt tgtatttggt tcgtttaaga gcaaacagta tatcaaatca tgataagaag 840

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attacaaaag caaatgtgtc agagtatttt aaagatatat atgaaacttt cggggaaaac 900
gctaaggaag caaaaaatta tttaaaagca gcaagcaggg ttataactgc tttaaaattg 960
atagaatttt ttaaagatca aaaaaacgaa aatgcacttg ctataaaaga aacattttta 1020
ccttgctatg ccaaaaaagc tttaatgatt aaaaaattta aaaaagatcc tttaaattta 1080
aaggaacaat tagttttaat taaacctttt attcaaacaa aacttcctta tgatatttgg 1140
aaattttggc aaaaaataaa aaatatttaa 1170

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<210> 16
<211> 1044
<212> DNA
<213> Campylobacter jejuni

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<220>
<221> CDS
<222> (1)..(1044)
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni strain OH4384 (ORF 5a
of lipooligosaccharide (LOS) biosynthesis locus)

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<400> 16
atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48
Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
1 5 10 15

ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
20 25 30

ata caa cga gat aaa atc gat tct tat tta cca aaa aaa act ctt gtg 144
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val
35 40 45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct 192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
50 55 60

att ata ggg gag ggg cat aaa gga tat ttt aat tat gat gaa aaa tct 240
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
65 70 75 80

aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa 288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
85 90 95

aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct 336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
100 105 110

atc caa aga ggt gtt ata gga tat aat gat tgt acc gat gga agt gaa 384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
115 120 125

gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata 432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
130 135 140

aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat 480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
145 150 155 160

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aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctt ata aaa ata gat gtg gat cat atc tat gat gct aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys	
180 185 190	
ctt tat aaa agc ttc tat ata cca aaa aac aaa tat gat gta gtt agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser	
195 200 205	
tat tca agg gtt gat att cac tat ttt aat gat aat ttt ttt ctt tgt	672
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys	
210 215 220	
aaa gat aat aat ggc aat ata ttg aaa gaa cca gga gat tgc ttg ctt	720
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu	
225 230 235 240	
atc aat aat tat aac tta aaa tgg aaa gaa gta tta att gac aga atc	768
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile	
245 250 255	
aat aac aat tgg aaa aaa gca aca aaa caa agt ttt tct tca aat ata	816
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile	
260 265 270	
cac tct tta gag caa tta aag tat aaa cac agg ata tta ttt cac act	864
His Ser Leu Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr	
275 280 285	
gaa tta aat aat tat cat ttt cct ttt tta aaa aaa cat aga gct caa	912
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln	
290 295 300	
gat att tat aaa tat aat tgg ata agt att gaa gaa ttt aaa aaa ttc	960
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe	
305 310 315 320	
tat tta caa aat att aat cat aaa ata gaa cct tct atg att tca aaa	1008
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys	
325 330 335	
gaa act cta aaa aaa ata ttc tta aca ttg ttt taa	1044
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe	
340 345	

<210> 17
 <211> 347
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni strain OH4384 (ORF 5a
 of lipooligosaccharide (LOS) biosynthesis locus)

<400> 17

Met	Leu	Phe	Gln	Ser	Tyr	Phe	Val	Lys	Ile	Ile	Cys	Leu	Phe	Ile	Pro
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			20					25					30		
Ile	Gln	Arg	Asp	Lys	Ile	Asp	Ser	Tyr	Leu	Pro	Lys	Lys	Thr	Leu	Val
		35					40					45			
Gln	Ile	Asn	Lys	Tyr	Asn	Asn	Glu	Asp	Leu	Ile	Lys	Leu	Asn	Lys	Ala
	50					55					60				
Ile	Ile	Gly	Glu	Gly	His	Lys	Gly	Tyr	Phe	Asn	Tyr	Asp	Glu	Lys	Ser
65					70					75				80	
Lys	Asp	Pro	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Ala	Phe	Ile	Arg	Val	Lys
				85					90					95	
Asn	Glu	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala
			100					105					110		
Ile	Gln	Arg	Gly	Val	Ile	Gly	Tyr	Asn	Asp	Cys	Thr	Asp	Gly	Ser	Glu
		115					120					125			
Glu	Ile	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Ser	Phe	Ile	Pro	Ile
	130					135					140				
Lys	Tyr	Pro	Tyr	Glu	Ile	Gln	Ile	Gln	Asn	Pro	Lys	Ser	Glu	Glu	Asn
145					150					155				160	
Lys	Leu	Tyr	Ser	Tyr	Tyr	Asn	Tyr	Val	Ala	Ser	Phe	Ile	Pro	Lys	Asp
				165					170					175	
Glu	Trp	Leu	Ile	Lys	Ile	Asp	Val	Asp	His	Ile	Tyr	Asp	Ala	Lys	Lys
			180					185					190		
Leu	Tyr	Lys	Ser	Phe	Tyr	Ile	Pro	Lys	Asn	Lys	Tyr	Asp	Val	Val	Ser
		195					200					205			
Tyr	Ser	Arg	Val	Asp	Ile	His	Tyr	Phe	Asn	Asp	Asn	Phe	Phe	Leu	Cys
	210					215					220				
Lys	Asp	Asn	Asn	Gly	Asn	Ile	Leu	Lys	Glu	Pro	Gly	Asp	Cys	Leu	Leu
225					230					235				240	
Ile	Asn	Asn	Tyr	Asn	Leu	Lys	Trp	Lys	Glu	Val	Leu	Ile	Asp	Arg	Ile
				245					250					255	
Asn	Asn	Asn	Trp	Lys	Lys	Ala	Thr	Lys	Gln	Ser	Phe	Ser	Ser	Asn	Ile
		260						265					270		
His	Ser	Leu	Glu	Gln	Leu	Lys	Tyr	Lys	His	Arg	Ile	Leu	Phe	His	Thr
		275					280					285			
Glu	Leu	Asn	Asn	Tyr	His	Phe	Pro	Phe	Leu	Lys	Lys	His	Arg	Ala	Gln
	290					295					300				
Asp	Ile	Tyr	Lys	Tyr	Asn	Trp	Ile	Ser	Ile	Glu	Glu	Phe	Lys	Lys	Phe
305					310					315					320
Tyr	Leu	Gln	Asn	Ile	Asn	His	Lys	Ile	Glu	Pro	Ser	Met	Ile	Ser	Lys
			325						330					335	
Glu	Thr	Leu	Lys	Lys	Ile	Phe	Leu	Thr	Leu	Phe					
		340						345							

<210> 18

<211> 1608

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1608)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:1

<400> 18

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1 5 10 15	
gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa	96
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys	
20 25 30	
aaa atc tac aat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac	144
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn	
35 40 45	
tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta	192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct	240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt	288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca	336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa	384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa	432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa	480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga	528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat	576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa	624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag	672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa	720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	

att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg	768
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg	816
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga	864
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	
275 280 285	
aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt	912
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg	
290 295 300	
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct	960
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala	
305 310 315 320	
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta	1008
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu	
325 330 335	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca	1056
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala	
340 345 350	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat	1104
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp	
355 360 365	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga	1152
Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg	
370 375 380	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg	1200
Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu	
385 390 395 400	
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa	1248
His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln	
405 410 415	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta	1296
Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu	
420 425 430	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt	1344
Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys	
435 440 445	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa	1392
Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys	
450 455 460	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca	1440
Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro	
465 470 475 480	

aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta 1488
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu
 485 490 495

ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata 1536
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile
 500 505 510

atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa 1584
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys
 515 520 525

aga gtt aat aat ata agc ttc tta 1608
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

<210> 19
 <211> 536
 <212> PRT
 <213> Campylobacter jejuni

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni O:1

<400> 19
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
 1 5 10 15
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
 20 25 30
 Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
 35 40 45
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val
 50 55 60
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro
 65 70 75 80
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser
 85 90 95
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro
 100 105 110
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu
 115 120 125
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln
 130 135 140
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys
 145 150 155 160
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg
 165 170 175
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn
 180 185 190
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln
 195 200 205
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln
 210 215 220
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln
 225 230 235 240
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp
 245 250 255
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu
 260 265 270

Asp	Ala	Leu	Thr	Leu	Glu	Asp	Phe	Lys	Lys	Ile	His	Tyr	Arg	His	Arg
	275						280					285			
Lys	Ile	Lys	Lys	Ile	Asn	Tyr	Thr	Met	Leu	Asp	Glu	Lys	Val	Ile	Arg
	290					295					300				
Glu	Ile	Leu	Asp	Lys	Phe	Lys	Leu	Ser	Gly	Lys	Lys	Met	Thr	Leu	Ala
305					310					315					320
Ile	Ile	Pro	Ala	Arg	Ala	Gly	Ser	Lys	Gly	Ile	Lys	Asn	Lys	Asn	Leu
				325					330					335	
Ala	Leu	Leu	His	Asp	Arg	Pro	Leu	Leu	Tyr	Tyr	Thr	Ile	Asn	Ala	Ala
			340					345					350		
Lys	Asn	Ser	Lys	Tyr	Val	Asp	Lys	Ile	Val	Leu	Ser	Ser	Asp	Gly	Asp
	355						360					365			
Asp	Ile	Leu	Glu	Tyr	Gly	Gln	Thr	Gln	Gly	Val	Asp	Val	Leu	Lys	Arg
	370					375					380				
Pro	Lys	Glu	Leu	Ala	Leu	Asp	Asp	Thr	Thr	Ser	Asp	Lys	Val	Val	Leu
385					390					395					400
His	Thr	Leu	Ser	Phe	Tyr	Lys	Asp	Tyr	Glu	Asn	Ile	Val	Leu	Leu	Gln
				405					410					415	
Pro	Thr	Ser	Pro	Leu	Arg	Thr	Asn	Val	His	Ile	Asp	Glu	Ala	Phe	Leu
			420					425					430		
Lys	Phe	Lys	Asn	Glu	Asn	Ser	Asn	Ala	Leu	Ile	Ser	Val	Val	Glu	Cys
	435						440					445			
Asp	Asn	Lys	Ile	Leu	Lys	Ala	Phe	Ile	Asp	Asp	Asn	Gly	Asn	Leu	Lys
	450					455					460				
Gly	Ile	Cys	Asp	Asn	Lys	Tyr	Pro	Phe	Met	Pro	Arg	Gln	Lys	Leu	Pro
465					470					475					480
Lys	Thr	Tyr	Met	Ser	Asn	Gly	Ala	Ile	Tyr	Ile	Val	Lys	Ser	Asn	Leu
				485					490					495	
Phe	Leu	Asn	Asn	Pro	Thr	Phe	Leu	Gln	Glu	Lys	Thr	Ser	Cys	Tyr	Ile
			500					505					510		
Met	Asp	Glu	Lys	Ala	Ser	Leu	Asp	Ile	Asp	Thr	Thr	Glu	Asp	Leu	Lys
	515						520					525			
Arg	Val	Asn	Asn	Ile	Ser	Phe	Leu								
	530					535									

<210> 20
 <211> 1056
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(1056)
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni O:10

<400> 20																
atg	cta	ttt	caa	tca	tac	ttt	gtg	aaa	ata	att	tgc	tta	ttc	atc	cct	48
Met	Leu	Phe	Gln	Ser	Tyr	Phe	Val	Lys	Ile	Ile	Cys	Leu	Phe	Ile	Pro	
1				5					10					15		
ttt	aga	aaa	att	aga	cat	aaa	ata	aaa	aaa	aca	ttt	tta	cta	aaa	aac	96
Phe	Arg	Lys	Ile	Arg	His	Lys	Ile	Lys	Lys	Thr	Phe	Leu	Leu	Lys	Asn	
			20					25					30			
ata	caa	cga	gat	aaa	atc	gat	tct	tat	cta	cca	aaa	aaa	act	ctt	ata	144
Ile	Gln	Arg	Asp	Lys	Ile	Asp	Ser	Tyr	Leu	Pro	Lys	Lys	Thr	Leu	Ile	
		35					40					45				

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct	192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50 55 60	
att ata ggg ggg ggg cat aaa gga tat ttt aat tat gat gaa aaa tct	240
Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65 70 75 80	
aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa	288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85 90 95	
aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct	336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100 105 110	
att caa aga ggt gtt ata gga tat aat gat tgc acc gat gga agt gaa	384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115 120 125	
gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata	432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130 135 140	
aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat	480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145 150 155 160	
aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctc ata aaa ata gat gtg gat cat tat tat gat gca aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180 185 190	
tta tat aag agt ttt tat ata cct aga aaa aat tat cat gta att agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195 200 205	
tac tct agg ata gat ttt ata ttt aat gaa gaa aaa ttt tat gtt tat	672
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210 215 220	
cgg aat aag gag ggg gag att tta aaa gct cct gga gat tgt tta gca	720
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225 230 235 240	
ata caa aac act aac tta ttt tgg aaa gaa ata ctt att gaa gat gat	768
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245 250 255	
aca ttt aag tgg aat act gca aaa aat aat ata gag aat gca aaa tca	816
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260 265 270	
tat gaa att tta aaa gtt aga aat aga att tat ttt act aca gaa ctt	864
Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu	
275 280 285	

aat aat tat cat ttt cca ttt ata aaa aat tat aga aaa aat gat tat	912
Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr	
290 295 300	
aag cag tta aat tgg gtt agc tta gat gat ttt att aaa aat tat aaa	960
Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys	
305 310 315 320	
gaa aaa tta aaa aat caa ata gat ttt aaa atg cta gaa tac aaa aca	1008
Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr	
325 330 335	
tta aaa aaa gtg tac aaa aag ctt aca tct tca gca agc gat aaa att	1056
Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile	
340 345 350	

<210> 21
 <211> 352
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni O:10

<400> 21

Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro	
1 5 10 15	
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn	
20 25 30	
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile	
35 40 45	
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50 55 60	
Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65 70 75 80	
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85 90 95	
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100 105 110	
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115 120 125	
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130 135 140	
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145 150 155 160	
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180 185 190	
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195 200 205	
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210 215 220	
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225 230 235 240	
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245 250 255	
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260 265 270	

Tyr	Glu	Ile	Leu	Lys	Val	Arg	Asn	Arg	Ile	Tyr	Phe	Thr	Thr	Glu	Leu
		275					280					285			
Asn	Asn	Tyr	His	Phe	Pro	Phe	Ile	Lys	Asn	Tyr	Arg	Lys	Asn	Asp	Tyr
	290					295					300				
Lys	Gln	Leu	Asn	Trp	Val	Ser	Leu	Asp	Asp	Phe	Ile	Lys	Asn	Tyr	Lys
305					310					315					320
Glu	Lys	Leu	Lys	Asn	Gln	Ile	Asp	Phe	Lys	Met	Leu	Glu	Tyr	Lys	Thr
			325						330					335	
Leu	Lys	Lys	Val	Tyr	Lys	Lys	Leu	Thr	Ser	Ser	Ala	Ser	Asp	Lys	Ile
			340					345						350	

<210> 22
 <211> 945
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(945)
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni O:36

<400> 22																
atg	ctt	aaa	aaa	atc	att	tct	tta	tat	aaa	aga	tac	tcg	att	tct	aaa	48
Met	Leu	Lys	Lys	Ile	Ile	Ser	Leu	Tyr	Lys	Arg	Tyr	Ser	Ile	Ser	Lys	
1				5					10					15		
aaa ttg gtt tta gat aat gag cat ttc att aag gaa aat aaa aac atc																96
Lys	Leu	Val	Leu	Asp	Asn	Glu	His	Phe	Ile	Lys	Glu	Asn	Lys	Asn	Ile	
			20					25					30			
tat gga aaa aaa cat aag ggc ttt ttt gac ttt gat gaa aag gct aag																144
Tyr	Gly	Lys	Lys	His	Lys	Gly	Phe	Phe	Asp	Phe	Asp	Glu	Lys	Ala	Lys	
		35				40						45				
gat gtg aaa tca ccc ctt aat cct tgg gga ttt atc agg gtt aaa aat																192
Asp	Val	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Gly	Phe	Ile	Arg	Val	Lys	Asn	
		50				55					60					
gaa gct tta acc cta aga gtt tct tta gaa agt ata cta cct gct tta																240
Glu	Ala	Leu	Thr	Leu	Arg	Val	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala	Leu	
65					70				75						80	
caa aga gga att ata gct tac aac gac tgt gat gat ggg agt gaa gag																288
Gln	Arg	Gly	Ile	Ile	Ala	Tyr	Asn	Asp	Cys	Asp	Asp	Gly	Ser	Glu	Glu	
			85				90							95		
ctt att tta gaa ttt tgc aag caa tat ccc aac ttc att gct aaa aaa																336
Leu	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Asn	Phe	Ile	Ala	Lys	Lys	
		100					105						110			
tat cct tat aaa gta gat cta gaa aat cct aaa aat gaa gaa aat aaa																384
Tyr	Pro	Tyr	Lys	Val	Asp	Leu	Glu	Asn	Pro	Lys	Asn	Glu	Glu	Asn	Lys	
		115				120						125				
ctt tac tct tat tac aat tgg gca gca tct ttt ata ccc tta gat gag																432
Leu	Tyr	Ser	Tyr	Tyr	Asn	Trp	Ala	Ala	Ser	Phe	Ile	Pro	Leu	Asp	Glu	
	130					135					140					

tgg ttt ata aaa atc gat gtg gat cat tac tac gat gcc aag aag ctt	480
Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu	
145 150 155 160	
tat aag agt ttt tat agg att gat caa gaa aat aaa gcc tta tgc tac	528
Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr	
165 170 175	
cca aga att aat ttt ata atc tta aat gga aat att tat gtg caa aat	576
Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn	
180 185 190	
agt gga aat tat gga ttc ata ggg ggg ggg gat caa ctc ttg att aaa	624
Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys	
195 200 205	
aga aga aat agt agc ttt ata gaa aga agg gtt tca aaa aaa agc caa	672
Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln	
210 215 220	
tgg ata gat cct aag gga ctt ata gaa gaa ctc tac tcc gag caa caa	720
Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
gtc tta tct caa gga gtg aaa ata cta caa gct ccc cta ctt cag tgg	768
Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp	
245 250 255	
cat ttt cct gcc tta aaa tac cgc cga aac gat tac caa caa tat tta	816
His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu	
260 265 270	
gat atc ttg agt tta gaa gaa ttt cag gcc ttt cat cgt aag agc aaa	864
Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys	
275 280 285	
gag gct aaa aaa ata gac ttt gcc atg cta aaa cgc cct gta atc gag	912
Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu	
290 295 300	
caa ata tta aag aaa ttt caa gga gag ata aaa	945
Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys	
305 310 315	

<210> 23

<211> 315

<212> PRT

<213> Campylobacter jejuni

<220>

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:36

<400> 23

Met Leu Lys Lys Ile Ile Ser Leu Tyr Lys Arg Tyr Ser Ile Ser Lys	
1 5 10 15	
Lys Leu Val Leu Asp Asn Glu His Phe Ile Lys Glu Asn Lys Asn Ile	
20 25 30	
Tyr Gly Lys Lys His Lys Gly Phe Phe Asp Phe Asp Glu Lys Ala Lys	
35 40 45	

Asp Val Lys Ser Pro Leu Asn Pro Trp Gly Phe Ile Arg Val Lys Asn
 50 55 60
 Glu Ala Leu Thr Leu Arg Val Ser Leu Glu Ser Ile Leu Pro Ala Leu
 65 70 75 80
 Gln Arg Gly Ile Ile Ala Tyr Asn Asp Cys Asp Asp Gly Ser Glu Glu
 85 90 95
 Leu Ile Leu Glu Phe Cys Lys Gln Tyr Pro Asn Phe Ile Ala Lys Lys
 100 105 110
 Tyr Pro Tyr Lys Val Asp Leu Glu Asn Pro Lys Asn Glu Glu Asn Lys
 115 120 125
 Leu Tyr Ser Tyr Tyr Asn Trp Ala Ala Ser Phe Ile Pro Leu Asp Glu
 130 135 140
 Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu
 145 150 155 160
 Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr
 165 170 175
 Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn
 180 185 190
 Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys
 195 200 205
 Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln
 210 215 220
 Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln
 225 230 235 240
 Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp
 245 250 255
 His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu
 260 265 270
 Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys
 275 280 285
 Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu
 290 295 300
 Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys
 305 310 315

<210> 24
 <211> 1608
 <212> DNA
 <213> *Campylobacter jejuni*

<220>
 <221> CDS
 <222> (1)..(1608)
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from *C. jejuni* NCTC 11168

<400> 24
 atg act ttg ttt tat aaa att ata gct ttt tta aga ttg ctt aaa att 48
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
 1 5 10 15
 gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa 96
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
 20 25 30
 aaa atc tac gat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac 144
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
 35 40 45

tca	aaa	gat	aca	aaa	tct	cct	tta	aat	cca	tg	gct	ttt	ata	aga	gta	192
Ser	Lys	Asp	Thr	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Ala	Phe	Ile	Arg	Val	
	50					55					60					
aaa	aat	gaa	gcc	act	act	tta	aga	gta	tca	ctt	gaa	agt	atg	tta	cct	240
Lys	Asn	Glu	Ala	Thr	Thr	Leu	Arg	Val	Ser	Leu	Glu	Ser	Met	Leu	Pro	
65					70					75					80	
gcc	ata	caa	aga	ggt	gtt	ata	gga	tat	aat	gat	tgt	act	gat	gga	agt	288
Ala	Ile	Gln	Arg	Gly	Val	Ile	Gly	Tyr	Asn	Asp	Cys	Thr	Asp	Gly	Ser	
				85					90					95		
gaa	gaa	att	att	ttg	gaa	ttt	tgc	aaa	caa	tac	cct	tcg	ttt	ata	cca	336
Glu	Glu	Ile	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Ser	Phe	Ile	Pro	
				100				105						110		
gta	aaa	tat	ccc	cat	gag	gtg	caa	att	gaa	aat	ccg	caa	agc	gaa	gaa	384
Val	Lys	Tyr	Pro	His	Glu	Val	Gln	Ile	Glu	Asn	Pro	Gln	Ser	Glu	Glu	
				115			120						125			
aat	aaa	ctt	cat	agt	tat	tat	aac	tat	gta	gct	agt	ttt	ata	ccg	caa	432
Asn	Lys	Leu	His	Ser	Tyr	Tyr	Asn	Tyr	Val	Ala	Ser	Phe	Ile	Pro	Gln	
	130					135					140					
gat	gag	tg	ctt	ata	aaa	ata	gat	gtg	gat	cat	tac	tat	gat	gca	aaa	480
Asp	Glu	Trp	Leu	Ile	Lys	Ile	Asp	Val	Asp	His	Tyr	Tyr	Asp	Ala	Lys	
145					150					155					160	
aaa	tta	tat	aag	agt	ttt	tat	atg	gca	tca	aaa	aat	act	gct	gtt	aga	528
Lys	Leu	Tyr	Lys	Ser	Phe	Tyr	Met	Ala	Ser	Lys	Asn	Thr	Ala	Val	Arg	
				165				170						175		
ttt	cca	aga	att	aat	ttt	tta	ata	cta	gat	aaa	att	gta	att	caa	aat	576
Phe	Pro	Arg	Ile	Asn	Phe	Leu	Ile	Leu	Asp	Lys	Ile	Val	Ile	Gln	Asn	
			180					185					190			
ata	gga	gaa	tgt	ggt	ttt	atc	gat	gga	ggg	gat	caa	ttg	tta	att	caa	624
Ile	Gly	Glu	Cys	Gly	Phe	Ile	Asp	Gly	Gly	Asp	Gln	Leu	Leu	Ile	Gln	
		195					200					205				
aag	tgc	aat	agt	gta	ttt	ata	gaa	aga	atg	gtt	tca	aag	caa	agt	cag	672
Lys	Cys	Asn	Ser	Val	Phe	Ile	Glu	Arg	Met	Val	Ser	Lys	Gln	Ser	Gln	
	210					215					220					
tg	att	gat	cct	gaa	aaa	act	gtg	aaa	gaa	ttg	tat	tct	gaa	cag	caa	720
Trp	Ile	Asp	Pro	Glu	Lys	Thr	Val	Lys	Glu	Leu	Tyr	Ser	Glu	Gln	Gln	
225					230					235					240	
att	ata	ccc	aaa	cat	ata	aaa	atc	tta	caa	gca	gaa	tta	ctt	caa	tg	768
Ile	Ile	Pro	Lys	His	Ile	Lys	Ile	Leu	Gln	Ala	Glu	Leu	Leu	Gln	Trp	
				245					250					255		
cat	ttt	cct	gct	tta	aaa	tat	cat	aga	aat	gat	tat	caa	aaa	cat	ttg	816
His	Phe	Pro	Ala	Leu	Lys	Tyr	His	Arg	Asn	Asp	Tyr	Gln	Lys	His	Leu	
			260					265					270			
gat	gct	tta	act	tta	gaa	gat	ttt	aaa	aaa	atc	cat	tat	aga	cat	aga	864
Asp	Ala	Leu	Thr	Leu	Glu	Asp	Phe	Lys	Lys	Ile	His	Tyr	Arg	His	Arg	
		275					280						285			

aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt	912
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg	
290 295 300	
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct	960
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala	
305 310 315 320	
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta	1008
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu	
325 330 335	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca	1056
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala	
340 345 350	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat	1104
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp	
355 360 365	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga	1152
Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg	
370 375 380	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg	1200
Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu	
385 390 395 400	
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa	1248
His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln	
405 410 415	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta	1296
Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu	
420 425 430	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt	1344
Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys	
435 440 445	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa	1392
Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys	
450 455 460	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca	1440
Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro	
465 470 475 480	
aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta	1488
Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu	
485 490 495	
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata	1536
Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile	
500 505 510	
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa	1584
Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys	
515 520 525	

aga gtt aat aat ata agc ttc tta
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

1608

<210> 25
 <211> 536
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni NCTC 11168

<400> 25
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
 1 5 10 15
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
 20 25 30
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
 35 40 45
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val
 50 55 60
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro
 65 70 75 80
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser
 85 90 95
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro
 100 105 110
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu
 115 120 125
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln
 130 135 140
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys
 145 150 155 160
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg
 165 170 175
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn
 180 185 190
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln
 195 200 205
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln
 210 215 220
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln
 225 230 235 240
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp
 245 250 255
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu
 260 265 270
 Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg
 275 280 285
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg
 290 295 300
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala
 305 310 315 320
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu
 325 330 335
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala
 340 345 350
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp
 355 360 365

Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg
 370 375 380
 Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu
 385 390 395 400
 His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln
 405 410 415
 Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu
 420 425 430
 Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys
 435 440 445
 Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys
 450 455 460
 Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro
 465 470 475 480
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu
 485 490 495
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile
 500 505 510
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys
 515 520 525
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

<210> 26
 <211> 906
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(906)
 <223> beta-1,3-galactosyltransferase from C. jejuni strain
 OH4384 (ORF 6a of lipooligosaccharide (LOS)
 biosynthesis locus)

<400> 26
 atg ttt aaa att tca atc atc tta cca act tat aat gtg gaa caa tat 48
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
 1 5 10 15
 ata gca agg gca ata gaa agc tgt atc aat cag act ttt aaa gat ata 96
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
 20 25 30
 gaa ata att gta gtt gat gat tgt gga aat gat aat agt ata aat ata 144
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile
 35 40 45
 gcc aaa gaa tac tct aaa aaa gac aaa aga ata aaa ata atc cac aat 192
 Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn
 50 55 60
 gaa aaa aac tta ggt ctt tta aga gca aga tat gaa ggt gtg aaa gta 240
 Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
 65 70 75 80
 gca aac tct cct tat ata atg ttt tta gat cct gat gat tat ttg gaa 288
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
 85 90 95

cta aat gct tgt gaa gag tgt ata aaa att tta gat gaa cag gat gaa	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu	
100 105 110	
gtt gat tta gtg ttt ttc aat gct att gtt gaa agt aat gtt att tca	384
Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser	
115 120 125	
tat aaa aag ttt gac ttt aat tct ggt ttt tat agc aaa aaa gag ttt	432
Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe	
130 135 140	
gta aaa aaa att att gca aag aaa aat tta tat tgg act atg tgg ggg	480
Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly	
145 150 155 160	
aaa ctt ata aga aag aaa ttg tat tta gaa gct ttt gcg agt tta aga	528
Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg	
165 170 175	
ctc gag aaa gat gtt aaa atc aat atg gct gaa gat gta ttg tta tat	576
Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr	
180 185 190	
tat cca atg tta agt caa gct caa aaa ata gca tat atg aac tgt aat	624
Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn	
195 200 205	
tta tat cat tac gtg cct aat aat aat tca att tgt aat act aag aat	672
Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn	
210 215 220	
gaa gtg ctt gtt aaa aat aat att caa gag ttg cag ttg gtt tta aac	720
Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn	
225 230 235 240	
tat tta agg caa aat tat att tta aac aag tat tgt agc gtt ctc tat	768
Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr	
245 250 255	
gtg cta att aaa tat ttg cta tat att caa ata tat aaa ata aaa aga	816
Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg	
260 265 270	
aca aaa tta atg gtt aca tta tta gct aaa ata aat att tta act tta	864
Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu	
275 280 285	
aaa att tta ttt aaa tat aaa aaa ttt tta aaa caa tgt taa	906
Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys	
290 295 300	

<210> 27
 <211> 301
 <212> PRT
 <213> Campylobacter jejuni

<220>

<223> beta-1,3-galactosyltransferase from C. jejuni strain
OH4384 (ORF 6a of lipooligosaccharide (LOS)
biosynthesis locus)

<400> 27

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Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
 1           5           10           15
Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
      20           25           30
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile
      35           40           45
Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn
      50           55           60
Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
      65           70           75           80
Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
      85           90           95
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu
      100          105          110
Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser
      115          120          125
Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe
      130          135          140
Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly
      145          150          155          160
Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg
      165          170          175
Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr
      180          185          190
Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn
      195          200          205
Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn
      210          215          220
Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn
      225          230          235          240
Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr
      245          250          255
Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg
      260          265          270
Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu
      275          280          285
Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys
      290          295          300
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<210> 28

<211> 912

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(912)

<223> Campylobacter glycosyltransferase B (CgtB) beta-1,3
galactosyltransferase from C. jejuni serotype O:2
(strain NCTC 11168)

<400> 28

atg agt caa att tcc atc ata cta cca act tat aat gtg gaa aaa tat	48
Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr	
1 5 10 15	
att gct aga gca tta gaa agt tgc att aac caa act ttt aaa gat ata	96
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile	
20 25 30	
gaa atc att gta gta gat gat tgt ggt aat gat aaa agt ata gat ata	144
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile	
35 40 45	
gct aaa gag tat gct agt aaa gat gat aga ata aaa atc ata cat aat	192
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn	
50 55 60	
gaa gag aat tta aag ctt tta aga gca aga tat gaa ggt gct aaa gta	240
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val	
65 70 75 80	
gca act tca cct tat atc atg ttt tta gat tct gat gat tat tta gaa	288
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu	
85 90 95	
ctt aat gct tgc gaa gaa tgt att aaa att ttg gat atg ggt ggg ggg	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly	
100 105 110	
ggt aaa att gat ttg ttg tgt ttt gaa gct ttt att acc aat gca aaa	384
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys	
115 120 125	
aaa tca ata aaa aaa tta aat ata aaa caa gga aaa tac aac aac aaa	432
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys	
130 135 140	
gaa ttt aca atg caa ata ctt aaa act aaa aat cca ttt tgg aca atg	480
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met	
145 150 155 160	
tgg gct aaa ata atc aaa aaa gat att tat tta aaa gcc ttc aac atg	528
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met	
165 170 175	
tta aat ctc aaa aaa gaa atc aaa ata aat atg gca gaa gat gcc tta	576
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu	
180 185 190	
tta tat tat cct ttg aca ata tta tct aat gaa ata ttt tac tta aca	624
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr	
195 200 205	
caa cct ttg tat acc cag cat gta aat agc aat tct ata aca aat aat	672
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn	
210 215 220	
att aat tct tta gaa gct aat att caa gaa cat aaa att gtt tta aat	720
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn	
225 230 235 240	

gtt tta aaa tca att aaa aat aaa aaa aca cct cta tat ttt cta att	768
Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile	
245 250 255	
ata tat tta tta aaa att caa tta ttg aaa tat gaa caa aat ttt aat	816
Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn	
260 265 270	
aaa aga aat ata aat ctt att tat tat aaa ata aat att tta tat caa	864
Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln	
275 280 285	
aaa tat caa ttc aaa tgg aaa aaa ttt tta tat aat tta att ccg taa	912
Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro	
290 295 300	

<210> 29
 <211> 303
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter glycosyltransferase B (CgtB) beta-1,3
 galactosyltransferase from C. jejuni serotype O:2
 (strain NCTC 11168)

<400> 29

Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr	
1 5 10 15	
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile	
20 25 30	
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile	
35 40 45	
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn	
50 55 60	
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val	
65 70 75 80	
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu	
85 90 95	
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly	
100 105 110	
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys	
115 120 125	
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys	
130 135 140	
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met	
145 150 155 160	
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met	
165 170 175	
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu	
180 185 190	
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr	
195 200 205	
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn	
210 215 220	
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn	
225 230 235 240	
Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile	
245 250 255	

Ile	Tyr	Leu	Leu	Lys	Ile	Gln	Leu	Leu	Lys	Tyr	Glu	Gln	Asn	Phe	Asn
		260					265						270		
Lys	Arg	Asn	Ile	Asn	Leu	Ile	Tyr	Tyr	Lys	Ile	Asn	Ile	Leu	Tyr	Gln
		275					280					285			
Lys	Tyr	Gln	Phe	Lys	Trp	Lys	Lys	Phe	Leu	Tyr	Asn	Leu	Ile	Pro	
	290					295					300				

<210> 30
 <211> 891
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(891)
 <223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 30																
atg	ttt	aaa	att	tca	atc	atc	ttg	cca	act	tat	aat	gtg	gaa	caa	tat	48
Met	Phe	Lys	Ile	Ser	Ile	Ile	Leu	Pro	Thr	Tyr	Asn	Val	Glu	Gln	Tyr	
1				5					10				15			
ata gca agg gca ata gaa agt tgt atc aat cag act ttt aaa aat ata															96	
Ile	Ala	Arg	Ala	Ile	Glu	Ser	Cys	Ile	Asn	Gln	Thr	Phe	Lys	Asn	Ile	
			20				25						30			
gaa ata att gta gtt gat gat tgt gga agt gac aaa agt ata gat ata															144	
Glu	Ile	Ile	Val	Val	Asp	Asp	Cys	Gly	Ser	Asp	Lys	Ser	Ile	Asp	Ile	
			35				40					45				
gtt aaa gaa tat gcc aaa aaa gat gat aga ata aaa atc ata cat aat															192	
Val	Lys	Glu	Tyr	Ala	Lys	Lys	Asp	Asp	Arg	Ile	Lys	Ile	Ile	His	Asn	
	50					55					60					
gaa gaa aat tta aaa ctt tta aga gct aga tat gaa ggt gta aaa gta															240	
Glu	Glu	Asn	Leu	Lys	Leu	Leu	Arg	Ala	Arg	Tyr	Glu	Gly	Val	Lys	Val	
	65				70					75				80		
gca aac tct cct tat ata atg ttt tta gat cct gat gat tat tta gaa															288	
Ala	Asn	Ser	Pro	Tyr	Ile	Met	Phe	Leu	Asp	Pro	Asp	Asp	Tyr	Leu	Glu	
				85				90						95		
ctt aat gct tgt gaa gaa tgt atg aaa att tta aaa aac aat gaa ata															336	
Leu	Asn	Ala	Cys	Glu	Glu	Cys	Met	Lys	Ile	Leu	Lys	Asn	Asn	Glu	Ile	
			100					105					110			
gat tta tta ttt ttt aat gca ttt gta ttg gaa aat aac aat aaa ata															384	
Asp	Leu	Leu	Phe	Phe	Asn	Ala	Phe	Val	Leu	Glu	Asn	Asn	Asn	Lys	Ile	
			115				120						125			
gaa aga aag ttg aat ttt caa gaa aaa tgt tat gta aaa aaa gat ttt															432	
Glu	Arg	Lys	Leu	Asn	Phe	Gln	Glu	Lys	Cys	Tyr	Val	Lys	Lys	Asp	Phe	
	130					135					140					
tta aaa gaa cta tta aaa act aaa aat tta ttt tgg aca gtg tgg gca															480	
Leu	Lys	Glu	Leu	Leu	Lys	Thr	Lys	Asn	Leu	Phe	Trp	Thr	Val	Trp	Ala	
	145				150					155					160	

aaa gtc ata aaa aaa gaa tta tat ctc aag gct gtt ggt tta ata tcg	528
Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser	
165 170 175	
cta gaa aat gct aaa ata aat atg gct gaa gat gtt tta tta tat tac	576
Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr	
180 185 190	
cct ttg ata aat att tca aat act ata ttt cac ttg agt aaa aat tta	624
Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu	
195 200 205	
tac aat tat caa ata aat aat ttc tct ata acc aaa aca tta aca ttg	672
Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu	
210 215 220	
caa aat ata aaa aca aat ata caa gaa caa gat aat gtt cta tat ctt	720
Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu	
225 230 235 240	
cta aag aag atg caa tat aat tac aat ttt aac tta act ttg ctt aaa	768
Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys	
245 250 255	
tta att gag tat ttt tta tta att gaa aaa tac tca tta tca agc aag	816
Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys	
260 265 270	
cga aat gtt ctt tgt ttt aaa atc aat att ttt ttt aaa aaa atc caa	864
Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln	
275 280 285	
ttt aaa ttt tat cgc ttg ctg aag atg	891
Phe Lys Phe Tyr Arg Leu Leu Lys Met	
290 295	

<210> 31
 <211> 297
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 31
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
 1 5 10 15
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile
 20 25 30
 Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile
 35 40 45
 Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn
 50 55 60
 Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
 65 70 75 80
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
 85 90 95
 Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile
 100 105 110

Asp Leu Leu Phe Phe Asn Ala Phe Val Leu Glu Asn Asn Asn Lys Ile
 115 120 125
 Glu Arg Lys Leu Asn Phe Gln Glu Lys Cys Tyr Val Lys Lys Asp Phe
 130 135 140
 Leu Lys Glu Leu Leu Lys Thr Lys Asn Leu Phe Trp Thr Val Trp Ala
 145 150 155 160
 Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser
 165 170 175
 Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr
 180 185 190
 Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu
 195 200 205
 Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu
 210 215 220
 Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu
 225 230 235 240
 Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys
 245 250 255
 Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys
 260 265 270
 Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln
 275 280 285
 Phe Lys Phe Tyr Arg Leu Leu Lys Met
 290 295

<210> 32
 <211> 295
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> lipid A biosynthesis acyltransferase from C.
 jejuni OH4384

<400> 32
 Met Lys Asn Ser Asp Arg Ile Tyr Leu Ser Leu Tyr Tyr Ile Leu Lys
 1 5 10 15
 Phe Phe Val Thr Phe Met Pro Asp Cys Ile Leu His Phe Leu Ala Leu
 20 25 30
 Ile Val Ala Arg Ile Ala Phe His Leu Asn Lys Lys His Arg Lys Ile
 35 40 45
 Ile Asn Thr Asn Leu Gln Ile Cys Phe Pro Gln Tyr Thr Gln Lys Glu
 50 55 60
 Arg Asp Lys Leu Ser Leu Lys Ile Tyr Glu Asn Phe Ala Gln Phe Gly
 65 70 75 80
 Ile Asp Cys Leu Gln Asn Gln Asn Thr Thr Lys Glu Lys Ile Leu Asn
 85 90 95
 Lys Val Asn Phe Ile Asn Glu Asn Phe Leu Ile Asp Ala Leu Ala Leu
 100 105 110
 Lys Arg Pro Ile Ile Phe Thr Thr Ala His Tyr Gly Asn Trp Glu Ile
 115 120 125
 Leu Ser Leu Ala Tyr Ala Ala Lys Tyr Gly Ala Ile Ser Ile Val Gly
 130 135 140
 Lys Lys Leu Lys Ser Glu Val Met Tyr Glu Ile Leu Ser Gln Ser Arg
 145 150 155 160
 Thr Gln Phe Asp Ile Glu Leu Ile Asp Lys Lys Gly Gly Ile Arg Gln
 165 170 175
 Met Leu Ser Ala Leu Lys Lys Glu Arg Ala Leu Gly Ile Leu Thr Asp
 180 185 190

Gln Asp Cys Val Glu Asn Glu Ser Val Arg Leu Lys Phe Phe Asn Lys
 195 200 205
 Glu Val Asn Tyr Gln Met Gly Ala Ser Leu Ile Ala Gln Arg Ser Asn
 210 215 220
 Ala Leu Ile Ile Pro Val Tyr Ala Tyr Lys Glu Gly Gly Lys Phe Cys
 225 230 235 240
 Ile Glu Phe Phe Lys Ala Lys Asp Ser Gln Asn Ala Ser Leu Glu Glu
 245 250 255
 Leu Thr Leu Tyr Gln Ala Gln Ser Cys Glu Glu Met Ile Lys Lys Arg
 260 265 270
 Pro Trp Glu Tyr Phe Phe Phe His Arg Arg Phe Ala Ser Tyr Asn Glu
 275 280 285
 Glu Ile Tyr Lys Gly Ala Lys
 290 295

<210> 33
 <211> 418
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> glycosyltransferase from C. jejuni OH4384 (ORF 3a
 of lipooligosaccharide (LOS) biosynthesis locus)

<400> 33
 Met Asn Leu Lys Gln Ile Ser Val Ile Ile Ile Val Lys Asn Ala Glu
 1 5 10 15
 Gln Thr Leu Leu Glu Cys Leu Asn Ser Leu Lys Asp Phe Asp Glu Ile
 20 25 30
 Ile Leu Leu Asn Asn Glu Ser Ser Asp Asn Thr Leu Lys Ile Ala Asn
 35 40 45
 Glu Phe Lys Lys Asp Phe Ala Asn Leu Tyr Ile Tyr His Asn Ala Phe
 50 55 60
 Ile Gly Phe Gly Ala Leu Lys Asn Leu Ala Leu Ser Tyr Ala Lys Asn
 65 70 75 80
 Asp Trp Ile Leu Ser Ile Asp Ala Asp Glu Val Leu Glu Asn Glu Cys
 85 90 95
 Ile Lys Glu Leu Lys Asn Leu Lys Leu Gln Glu Asp Asn Ile Ile Ala
 100 105 110
 Leu Ser Arg Lys Asn Leu Tyr Lys Gly Glu Trp Ile Lys Ala Cys Gly
 115 120 125
 Trp Trp Pro Asp Tyr Val Leu Arg Ile Phe Asn Lys Asn Phe Thr Arg
 130 135 140
 Phe Asn Asp Asn Leu Val His Glu Ser Leu Val Leu Pro Ser Asn Ala
 145 150 155 160
 Lys Lys Ile Tyr Leu Lys Asn Gly Leu Lys His Tyr Ser Tyr Lys Asp
 165 170 175
 Ile Ser His Leu Ile Asp Lys Met Gln Tyr Tyr Ser Ser Leu Trp Ala
 180 185 190
 Lys Gln Asn Ile His Lys Lys Ser Gly Val Leu Lys Ala Asn Leu Arg
 195 200 205
 Ala Phe Trp Thr Phe Phe Arg Asn Tyr Phe Leu Lys Asn Gly Phe Leu
 210 215 220
 Tyr Gly Tyr Lys Gly Phe Ile Ile Ser Val Cys Ser Ala Leu Gly Thr
 225 230 235 240
 Phe Phe Lys Tyr Met Lys Leu Tyr Glu Leu Gln Arg Gln Lys Pro Lys
 245 250 255
 Thr Cys Ala Leu Ile Ile Ile Thr Tyr Asn Gln Lys Glu Arg Leu Lys
 260 265 270

Leu Val Leu Asp Ser Val Lys Asn Leu Ala Phe Leu Pro Asn Glu Val
 275 280 285
 Leu Ile Ala Asp Asp Gly Ser Lys Glu Asp Thr Ala Arg Leu Ile Glu
 290 295 300
 Glu Tyr Gln Lys Asp Phe Pro Cys Pro Leu Lys His Ile Trp Gln Glu
 305 310 315 320
 Asp Glu Gly Phe Lys Leu Ser Lys Ser Arg Asn Lys Thr Ile Lys Asn
 325 330 335
 Ala Asp Ser Glu Tyr Ile Ile Val Ile Asp Gly Asp Met Ile Leu Glu
 340 345 350
 Lys Asp Phe Ile Lys Glu His Leu Glu Phe Ala Gln Arg Lys Leu Phe
 355 360 365
 Leu Gln Gly Ser Arg Val Ile Leu Asn Lys Lys Glu Ser Glu Glu Ile
 370 375 380
 Leu Asn Lys Asp Asp Tyr Arg Ile Ile Phe Asn Lys Lys Asp Phe Lys
 385 390 395 400
 Ser Ser Lys Asn Ser Phe Leu Ala Lys Ile Phe Tyr Ser Leu Ser Lys
 405 410 415
 Lys Arg

<210> 34
 <211> 389
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> glycosyltransferase of C. jejuni OH4384 (ORF 4a of
 lipooligosaccharide (LOS) biosynthesis locus)

<400> 34
 Met Lys Lys Ile Gly Val Val Ile Pro Ile Tyr Asn Val Glu Lys Tyr
 1 5 10 15
 Leu Arg Glu Cys Leu Asp Ser Val Ile Asn Gln Thr Tyr Thr Asn Leu
 20 25 30
 Glu Ile Ile Leu Val Asn Asp Gly Ser Thr Asp Glu His Ser Leu Asn
 35 40 45
 Ile Ala Lys Glu Tyr Thr Leu Lys Asp Lys Arg Ile Thr Leu Phe Asp
 50 55 60
 Lys Lys Asn Gly Gly Leu Ser Ser Ala Arg Asn Ile Gly Ile Glu Tyr
 65 70 75 80
 Phe Ser Gly Glu Tyr Lys Leu Lys Asn Lys Thr Gln His Ile Lys Glu
 85 90 95
 Asn Ser Leu Ile Glu Phe Gln Leu Asp Gly Asn Asn Pro Tyr Asn Ile
 100 105 110
 Tyr Lys Ala Tyr Lys Ser Ser Gln Ala Phe Asn Asn Glu Lys Asp Leu
 115 120 125
 Thr Asn Phe Thr Tyr Pro Ser Ile Asp Tyr Ile Ile Phe Leu Asp Ser
 130 135 140
 Asp Asn Tyr Trp Lys Leu Asn Cys Ile Glu Glu Cys Val Ile Arg Met
 145 150 155 160
 Lys Asn Val Asp Val Leu Trp Phe Asp His Asp Cys Thr Tyr Glu Asp
 165 170 175
 Asn Ile Lys Asn Lys His Lys Lys Thr Arg Met Glu Ile Phe Asp Phe
 180 185 190
 Lys Lys Glu Cys Ile Ile Thr Pro Lys Glu Tyr Ala Asn Arg Ala Leu
 195 200 205
 Ser Val Gly Ser Arg Asp Ile Ser Phe Gly Trp Asn Gly Met Ile Asp
 210 215 220
 Phe Asn Phe Leu Lys Gln Ile Lys Leu Lys Phe Ile Asn Phe Ile Ile
 225 230 235 240

Gly	Ala	Cys	Val	Leu	Glu	Arg	His	Phe	Thr	Asp	Ser	Met	His	Arg	Ser
225					230					235					240
Gly	Pro	Asp	Ile	Val	Cys	Ser	Met	Asp	Thr	Gln	Ala	Leu	Lys	Glu	Leu
				245					250					255	
Ile	Ile	Gln	Ser	Glu	Gln	Met	Ala	Ile	Met	Arg	Gly	Asn	Asn	Glu	Ser
			260				265						270		
Lys	Lys	Ala	Ala	Lys	Gln	Glu	Gln	Val	Thr	Ile	Asp	Phe	Ala	Phe	Ala
		275					280					285			
Ser	Val	Val	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Gly	Glu	Val	Leu	Ser	Met
	290					295					300				
Asp	Asn	Ile	Trp	Val	Lys	Arg	Pro	Gly	Leu	Gly	Gly	Ile	Ser	Ala	Ala
305					310					315					320
Glu	Phe	Glu	Asn	Ile	Leu	Gly	Lys	Lys	Ala	Leu	Arg	Asp	Ile	Glu	Asn
			325						330					335	
Asp	Thr	Gln	Leu	Ser	Tyr	Glu	Asp	Phe	Ala						
			340					345							

<210> 36
 <211> 352
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> enzyme involved in sialic acid biosynthesis from
 C. jejuni OH4384 (ORF 9a of lipooligosaccharide (LOS)
 biosynthesis locus)

<400> 36

Met	Tyr	Arg	Val	Gln	Asn	Ser	Ser	Glu	Phe	Glu	Leu	Tyr	Ile	Phe	Ala
1				5					10					15	
Thr	Gly	Met	His	Leu	Ser	Lys	Asn	Phe	Gly	Tyr	Thr	Val	Lys	Glu	Leu
			20					25					30		
Tyr	Lys	Asn	Gly	Phe	Lys	Asn	Ile	Tyr	Glu	Phe	Ile	Asn	Tyr	Asp	Lys
		35					40					45			
Tyr	Phe	Ser	Thr	Asp	Lys	Ala	Leu	Ala	Thr	Thr	Ile	Asp	Gly	Phe	Ser
	50					55					60				
Arg	Tyr	Val	Asn	Glu	Leu	Lys	Pro	Asp	Leu	Ile	Val	Val	His	Gly	Asp
	65				70					75					80
Arg	Ile	Glu	Pro	Leu	Ala	Ala	Ala	Ile	Val	Gly	Ala	Leu	Asn	Asn	Ile
				85					90					95	
Leu	Val	Ala	His	Ile	Glu	Gly	Gly	Glu	Ile	Ser	Gly	Thr	Ile	Asp	Asp
			100					105					110		
Ser	Leu	Arg	His	Ala	Ile	Ser	Lys	Leu	Ala	His	Ile	His	Leu	Val	Asn
		115					120					125			
Asp	Glu	Phe	Ala	Lys	Arg	Arg	Leu	Met	Gln	Leu	Gly	Glu	Asp	Glu	Lys
	130					135					140				
Ser	Ile	Phe	Ile	Ile	Gly	Ser	Pro	Asp	Leu	Glu	Leu	Leu	Asn	Asp	Asn
	145				150					155					160
Lys	Ile	Ser	Leu	Asn	Glu	Ala	Lys	Lys	Tyr	Tyr	Asp	Ile	Asn	Tyr	Glu
			165						170					175	
Asn	Tyr	Ala	Leu	Leu	Met	Phe	His	Pro	Val	Thr	Thr	Glu	Ile	Thr	Ser
		180						185					190		
Ile	Lys	Asn	Gln	Ala	Asp	Asn	Leu	Val	Lys	Ala	Leu	Ile	Gln	Ser	Asn
		195					200					205			
Lys	Asn	Tyr	Ile	Val	Ile	Tyr	Pro	Asn	Asn	Asp	Leu	Gly	Phe	Glu	Leu
	210					215					220				
Ile	Leu	Gln	Ser	Tyr	Glu	Glu	Leu	Lys	Asn	Asn	Pro	Arg	Phe	Lys	Leu
225					230					235					240
Phe	Pro	Ser	Leu	Arg	Phe	Glu	Tyr	Phe	Ile	Thr	Leu	Leu	Lys	Asn	Ala
			245						250					255	

Asp Phe Ile Ile Gly Asn Ser Ser Cys Ile Leu Lys Glu Ala Leu Tyr
 260 265 270
 Leu Lys Thr Ala Gly Ile Leu Val Gly Ser Arg Gln Asn Gly Arg Leu
 275 280 285
 Gly Asn Glu Asn Thr Leu Lys Val Asn Ala Asn Ser Asp Glu Ile Leu
 290 295 300
 Lys Ala Ile Asn Thr Ile His Lys Lys Gln Asp Leu Phe Ser Ala Lys
 305 310 315 320
 Leu Glu Ile Leu Asp Ser Ser Lys Leu Phe Phe Glu Tyr Leu Gln Ser
 325 330 335
 Gly Glu Phe Phe Lys Leu Asn Thr Gln Lys Val Phe Lys Asp Ile Lys
 340 345 350

<210> 37
 <211> 221
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> CMP-sialic acid synthetase from C. jejuni OH4384
 (ORF 10a of lipooligosaccharide (LOS) biosynthesis
 locus)

<400> 37
 Met Ser Leu Ala Ile Ile Pro Ala Arg Gly Gly Ser Lys Gly Ile Lys
 1 5 10 15
 Asn Lys Asn Leu Val Leu Leu Asn Asn Lys Pro Leu Ile Tyr Tyr Thr
 20 25 30
 Ile Lys Ala Ala Leu Asn Thr Lys Ser Ile Ser Lys Val Val Ser
 35 40 45
 Ser Asp Ser Asp Glu Ile Leu Asn Tyr Ala Lys Ser Gln Asn Val Asp
 50 55 60
 Ile Leu Lys Arg Pro Ile Ser Leu Ala Gln Asp Asn Thr Thr Ser Asp
 65 70 75 80
 Lys Val Leu Leu His Ala Leu Lys Phe Tyr Lys Asp Tyr Glu Asp Val
 85 90 95
 Val Phe Leu Gln Pro Thr Ser Pro Leu Arg Thr Asn Ile His Ile Asp
 100 105 110
 Glu Ala Phe Asn Leu Tyr Lys Asn Ser Asn Ala Asn Ala Leu Ile Ser
 115 120 125
 Val Ser Glu Cys Asp Asn Lys Ile Leu Lys Ala Phe Val Cys Asn Glu
 130 135 140
 Tyr Gly Asp Leu Ala Gly Ile Cys Asn Asp Glu Tyr Pro Phe Met Pro
 145 150 155 160
 Arg Gln Lys Leu Pro Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile
 165 170 175
 Leu Lys Ile Lys Glu Phe Leu Asn Asn Pro Ser Phe Leu Gln Ser Lys
 180 185 190
 Thr Lys His Phe Leu Met Asp Glu Ser Ser Ser Leu Asp Ile Asp Cys
 195 200 205
 Leu Glu Asp Leu Lys Lys Ala Glu Gln Ile Trp Lys Lys
 210 215 220

<210> 38
 <211> 277
 <212> PRT
 <213> Campylobacter jejuni

<220>

<223> acetyltransferase from *C. jejuni* OH4384 (ORF 11a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 38

```
Met Glu Lys Ile Thr Leu Lys Cys Asn Lys Asn Ile Leu Asn Leu Leu
 1           5           10           15
Lys Gln Tyr Asn Ile Tyr Thr Lys Thr Tyr Ile Glu Asn Pro Arg Arg
          20           25           30
Phe Ser Arg Leu Lys Thr Lys Asp Phe Ile Thr Phe Pro Leu Glu Asn
          35           40           45
Asn Gln Leu Glu Ser Val Ala Gly Leu Gly Ile Glu Glu Tyr Cys Ala
 50           55           60
Phe Lys Phe Ser Asn Ile Leu His Glu Met Asp Ser Phe Ser Phe Ser
 65           70           75           80
Gly Ser Phe Leu Pro His Tyr Thr Lys Val Gly Arg Tyr Cys Ser Ile
          85           90           95
Ser Asp Gly Val Ser Met Phe Asn Phe Gln His Pro Met Asp Arg Ile
          100          105          110
Ser Thr Ala Ser Phe Thr Tyr Glu Thr Asn His Ser Phe Ile Asn Asp
          115          120          125
Ala Cys Gln Asn His Ile Asn Lys Thr Phe Pro Ile Val Asn His Asn
 130          135          140
Pro Ser Ser Ser Ile Thr His Leu Ile Ile Gln Asp Asp Val Trp Ile
 145          150          155          160
Gly Lys Asp Val Leu Leu Lys Gln Gly Ile Thr Leu Gly Thr Gly Cys
          165          170          175
Val Ile Gly Gln Arg Ala Val Val Thr Lys Asp Val Pro Pro Tyr Ala
          180          185          190
Ile Val Ala Gly Ile Pro Ala Lys Ile Ile Lys Tyr Arg Phe Asp Glu
          195          200          205
Lys Thr Ile Glu Arg Leu Leu Lys Ile Gln Trp Trp Lys Tyr His Phe
 210          215          220
Ala Asp Phe Tyr Asp Ile Asp Leu Asn Leu Lys Ile Asn Gln Tyr Leu
 225          230          235          240
Asp Leu Leu Glu Glu Lys Ile Ile Lys Lys Ser Ile Ser Tyr Tyr Asn
          245          250          255
Pro Asn Lys Leu Tyr Phe Arg Asp Ile Leu Glu Leu Lys Ser Lys Lys
          260          265          270
Ile Phe Asn Leu Phe
          275
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<210> 39

<211> 270

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> glycosyltransferase from *C. jejuni* OH4384 (ORF 12a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 39

```
Met Pro Gln Leu Ser Ile Ile Ile Pro Leu Phe Asn Ser Cys Asp Phe
 1           5           10           15
Ile Ser Arg Ala Leu Gln Ser Cys Ile Asn Gln Thr Leu Lys Asp Ile
          20           25           30
Glu Ile Leu Ile Ile Asp Asp Lys Ser Lys Asp Asn Ser Leu Asn Met
          35           40           45
Val Leu Glu Phe Ala Lys Lys Asp Pro Arg Ile Lys Ile Phe Gln Asn
          50           55           60
```


Glu	Glu	Asn	Leu	Gly	Thr	Phe	Ala	Ser	Arg	Asn	Leu	Gly	Val	Leu	His
65					70					75					80
Ser	Ser	Ser	Asp	Phe	Ile	Met	Phe	Leu	Asp	Ser	Asp	Asp	Phe	Leu	Thr
			85						90					95	
Pro	Asp	Ala	Cys	Glu	Ile	Ala	Phe	Lys	Glu	Met	Lys	Lys	Gly	Phe	Asp
			100					105					110		
Leu	Leu	Cys	Phe	Asp	Ala	Phe	Val	His	Arg	Val	Lys	Thr	Lys	Gln	Phe
		115					120					125			
Tyr	Arg	Phe	Lys	Gln	Asp	Glu	Val	Phe	Asn	Gln	Lys	Glu	Phe	Leu	Glu
	130					135					140				
Phe	Leu	Ser	Lys	Gln	Arg	His	Phe	Cys	Trp	Ser	Val	Trp	Ala	Lys	Cys
145				150						155					160
Phe	Lys	Lys	Asp	Ile	Ile	Leu	Lys	Ser	Phe	Glu	Lys	Ile	Lys	Ile	Asp
			165						170					175	
Glu	Arg	Leu	Asn	Tyr	Gly	Glu	Asp	Val	Leu	Phe	Cys	Tyr	Ile	Tyr	Phe
			180					185					190		
Met	Phe	Cys	Glu	Lys	Ile	Ala	Val	Phe	Lys	Thr	Cys	Ile	Tyr	His	Tyr
		195				200						205			
Glu	Phe	Asn	Pro	Asn	Gly	Arg	Tyr	Glu	Asn	Lys	Asn	Lys	Glu	Ile	Leu
	210				215						220				
Asn	Gln	Asn	Tyr	His	Asp	Lys	Lys	Lys	Ser	Asn	Glu	Ile	Ile	Lys	Lys
225				230						235					240
Leu	Ser	Lys	Glu	Phe	Ala	His	Asp	Glu	Phe	His	Gln	Lys	Leu	Phe	Glu
			245					250						255	
Val	Leu	Lys	Arg	Glu	Glu	Ala	Gly	Val	Lys	Asn	Arg	Leu	Lys		
		260					265					270			

<210> 40
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ42 primer in
 heptosyltransferase-II used to amplify LPS core
 biosynthesis locus

<400> 40
 gccattaccg tatcgccctaa ccagg 25

<210> 41
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ43 primer in
 heptosyltransferase-I used to amplify LPS core
 biosynthesis locus

<400> 41
 aaagaatacg aatttgctaa agagg 25

<210> 42
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-106 3'
 primer used to amplify and clone ORF 5a

<400> 42
 cctagggtcga cttaaaacaa tgtaagaat atttttttta g 41

<210> 43
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-157 5'
 primer used to amplify and clone ORF 5a

<400> 43
 cttaggaggt catatgctat ttcaatcata ctttgtg 37

<210> 44
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-105 3'
 primer used to amplify and clone ORF 6a

<400> 44
 cctagggtcga cctctaaaaa aaatattctt aacattg 37

<210> 45
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-133 5'
 primer used to amplify and clone ORF 6a

<400> 45
 cttaggaggt catatgttta aaatttcaat catcttacc 39

<210> 46
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-131 5'
 primer used to amplify and clone ORF 7a

<400> 46
 cttaggaggt catatgaaaa aagttattat tgctggaaat g 41

<210> 47
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-132 3'
 primer used to amplify and clone ORF 7a

<400> 47
 cctaggtcga cttattttcc tttgaaataa tgctttatat c

41

<210> 48
 <211> 322
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
 from C. jejuni OH4384

<400> 48
 Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met
 1 5 10 15
 Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn
 20 25 30
 Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe
 35 40 45
 Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe
 50 55 60
 Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu
 65 70 75 80
 Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe
 85 90 95
 Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn
 100 105 110
 Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys
 115 120 125
 Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg
 130 135 140
 Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr
 145 150 155 160
 Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile
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 Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly
 180 185 190
 Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile
 195 200 205
 Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala
 210 215 220
 Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn
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 Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn
 245 250 255
 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn
 260 265 270
 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu
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 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val
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 35 40 45
 Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu
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 Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val
 65 70 75 80
 Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu
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 Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys
 100 105 110
 Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser
 115 120 125
 Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly
 130 135 140
 Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe
 145 150 155 160
 Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys
 165 170 175
 Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys
 180 185 190
 Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe
 195 200 205
 Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala
 210 215 220
 Leu Lys Ser Arg Lys Trp Asp
 225 230